



IFWO

RAW SEQUENCE LISTING

DATE: 08/30/2004

PATENT APPLICATION: US/10/828,920A

TIME: 14:53:30

Input Set : A:\66821-281

Output Set: N:\CRF4\08302004\J828920A.raw

5 <110> APPLICANT: Reed, John C.
 7 <120> TITLE OF INVENTION: Novel Card Proteins Involved in Cell Death Regulation
 9 <130> FILE REFERENCE: P-LJ 3650
 11 <140> CURRENT APPLICATION NUMBER: 10/828,920A
 12 <141> CURRENT FILING DATE: 2004-04-20
 14 <150> PRIOR APPLICATION NUMBER: 09/388,221
 15 <151> PRIOR FILING DATE: 1999-09-01
 17 <160> NUMBER OF SEQ ID NOS: 30
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 22 <210> SEQ ID NO: 1
 24 <211> LENGTH: 4422
 26 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
 32 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 36 <222> LOCATION: (1)..(4422)
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46	1 5 10 15	
50	aag aag gag gag ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg	96
52	Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala	
54	20 25 30	
58	cac tcc agg agc tct tct ggt gag aca ccc gct cag cca gag aag acg	144
60	His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr	
62	35 40 45	
66	agt ggc atg gag gtg gcc tct tac ctg gtg gct cag tat ggg gag cag	192
68	Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln	
70	50 55 60	
74	cgg gcc tgg gac cta gcc ctc cat acc tgg gag cag atg ggg ctg agg	240
76	Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg	
78	65 70 75 80	
82	tca ctg tgc gcc caa gcc cag gaa ggg gca ggc cac tct ccc tca ttc	288
84	Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe	
86	85 90 95	
90	ccc tac agc cca agt gaa ccc cac ctg ggg tct ccc agc caa ccc acc	336
92	Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr	
94	100 105 110	
98	tcc acc gca gtg cta atg ccc tgg atc cat gaa ttg ccg gcg ggg tgc	384
100	Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys	
102	115 120 125	
106	acc cag ggc tca gag aga agg gtt ttg aga cag ctg cct gac aca tct	432
108	Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser	



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116 Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu
118 145      150      155      160
122 cca agc tcc cca gac cat gag tct cca agc cag gag tca ccc aac gcc 528
124 Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala
126      165      170      175
130 ccc aca tcc aca gca gtg ctg ggg agc tgg gga tcc cca cct cag ccc 576
132 Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro
134      180      185      190
138 agc cta gca ccc aga gag cag gag gct cct ggg acc caa tgg cct ctg 624
140 Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu
142      195      200      205
146 gat gaa acg tca gga att tac tac aca gaa atc aga gaa aga gag aga 672
148 Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg
150      210      215      220
154 gag aaa tca gag aaa ggc agg ccc cca tgg gca gcg gtg gta gga acg 720
156 Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr
158 225      230      235      240
162 ccc cca cag gcg cac acc agc cta cag ccc cac cac cac cca tgg gag 768
164 Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu
166      245      250      255
170 cct tct gtg aga gag agc ctc tgt tcc aca tgg ccc tgg aaa aat gag 816
172 Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu
174      260      265      270
178 gat ttt aac caa aaa ttc aca cag ctg cta ctt cta caa aga cct cac 864
180 Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His
182      275      280      285
186 ccc aga agc caa gat ccc ctg gtc aag aga agc tgg cct gat tat gtg 912
188 Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val
190      290      295      300
194 gag gag aat cga gga cat tta att gag atc aga gac tta ttt ggc cca 960
196 Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro
198 305      310      315      320
202 ggc ctg gat acc caa gaa cct cgc ata gtc ata ctg cag ggg gct gct 1008
204 Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala
206      325      330      335
210 gga att ggg aag tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg 1056
212 Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly
214      340      345      350
218 aga ggc cag ctg tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc 1104
220 Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser
222      355      360      365
226 tgc aga gag ctg gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc 1152
228 Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile
230      370      375      380
234 gga aaa gat ggg aca gcc act ccg gct ccc att aga cag atc ctg tct 1200
236 Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser
238 385      390      395      400

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244	Arg	Pro	Glu	Arg	Leu	Leu	Phe	Ile	Leu	Asp	Gly	Val	Asp	Glu	Pro	Gly	
246				405					410					415			
250	tgg	gtc	ttg	cag	gag	ccg	agt	tct	gag	ctc	tgt	ctg	cac	tgg	agc	cag	1296
252	Trp	Val	Leu	Gln	Glu	Pro	Ser	Ser	Glu	Leu	Cys	Leu	His	Trp	Ser	Gln	
254				420					425					430			
258	cca	cag	ccg	gcg	gat	gca	ctg	ctg	ggc	agt	ttg	ctg	ggg	aaa	act	ata	1344
260	Pro	Gln	Pro	Ala	Asp	Ala	Leu	Leu	Gly	Ser	Leu	Leu	Gly	Lys	Thr	Ile	
262				435					440					445			
266	ctt	ccc	gag	gca	tcc	ttc	ctg	atc	acg	gct	cgg	acc	aca	gct	ctg	cag	1392
268	Leu	Pro	Glu	Ala	Ser	Phe	Leu	Ile	Thr	Ala	Arg	Thr	Thr	Ala	Leu	Gln	
270		450					455				460						
274	aac	ctc	att	cct	tct	ttg	gag	cag	gca	cgt	tgg	gta	gag	gtc	ctg	ggg	1440
276	Asn	Leu	Ile	Pro	Ser	Leu	Glu	Gln	Ala	Arg	Trp	Val	Glu	Val	Leu	Gly	
278	465					470					475					480	
282	ttc	tct	gag	tcc	agc	agg	aag	gaa	tat	ttc	tac	aga	tat	ttc	aca	gat	1488
284	Phe	Ser	Glu	Ser	Ser	Arg	Lys	Glu	Tyr	Phe	Tyr	Arg	Tyr	Phe	Thr	Asp	
286				485					490					495			
290	gaa	agg	caa	gca	att	aga	gcc	ttt	agg	ttg	gtc	aaa	tca	aac	aaa	gag	1536
292	Glu	Arg	Gln	Ala	Ile	Arg	Ala	Phe	Arg	Leu	Val	Lys	Ser	Asn	Lys	Glu	
294				500					505					510			
298	ctc	tgg	gcc	ctg	tgt	ctt	gtg	ccc	tgg	gtg	tcc	tgg	ctg	gcc	tgc	act	1584
300	Leu	Trp	Ala	Leu	Cys	Leu	Val	Pro	Trp	Val	Ser	Trp	Leu	Ala	Cys	Thr	
302			515				520					525					
306	tgc	ctg	atg	cag	cag	atg	aag	cgg	aag	gaa	aaa	ctc	aca	ctg	act	tcc	1632
308	Cys	Leu	Met	Gln	Gln	Met	Lys	Arg	Lys	Glu	Lys	Leu	Thr	Leu	Thr	Ser	
310		530				535					540						
314	aag	acc	acc	aca	acc	ctc	tgt	cta	cat	tac	ctt	gcc	cag	gct	ctc	caa	1680
316	Lys	Thr	Thr	Thr	Thr	Cys	Leu	His	Tyr	Leu	Ala	Gln	Ala	Leu	Gln		
318	545					550					555					560	
322	gct	cag	cca	ttg	gga	ccc	cag	ctc	aga	gac	ctc	tgc	tct	ctg	gct	gct	1728
324	Ala	Gln	Pro	Leu	Gly	Pro	Gln	Leu	Arg	Asp	Leu	Cys	Ser	Leu	Ala	Ala	
326				565					570					575			
330	gag	ggc	atc	tgg	caa	aaa	aag	acc	ctt	ttc	agt	cca	gat	gac	ctc	agg	1776
332	Glu	Gly	Ile	Trp	Gln	Lys	Lys	Thr	Leu	Phe	Ser	Pro	Asp	Asp	Leu	Arg	
334				580					585					590			
338	aag	cat	ggg	tta	gat	ggg	gcc	atc	atc	tcc	acc	ttc	ttg	aag	atg	ggg	1824
340	Lys	His	Gly	Leu	Asp	Gly	Ala	Ile	Ile	Ser	Thr	Phe	Leu	Lys	Met	Gly	
342				595				600						605			
346	att	ctt	caa	gag	cac	ccc	atc	cct	ctg	agc	tac	agc	ttc	att	cac	ctc	1872
348	Ile	Leu	Gln	Glu	His	Pro	Ile	Pro	Leu	Ser	Tyr	Ser	Phe	Ile	His	Leu	
350		610				615								620			
354	tgt	ttc	caa	gag	ttc	ttt	gca	gca	atg	tcc	tat	gtc	ttg	gag	gat	gag	1920
356	Cys	Phe	Gln	Glu	Phe	Phe	Ala	Ala	Met	Ser	Tyr	Val	Leu	Glu	Asp	Glu	
358	625					630					635					640	
362	aag	ggg	aga	ggg	aaa	cat	tct	aat	tgc	atc	ata	gat	ttg	gaa	aag	acg	1968
364	Lys	Gly	Arg	Gly	Lys	His	Ser	Asn	Cys	Ile	Ile	Asp	Leu	Glu	Lys	Thr	
366				645					650					655			
370	cta	gaa	gca	tat	gga	ata	cat	ggc	ctg	ttt	ggg	gca	tca	acc	aca	cgt	2016

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372 Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg
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378 ttc cta ttg ggc ctg tta agt gat gag ggg gag aga gag atg gag aac 2064
380 Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn
382          675          680          685
386 atc ttt cac tgc cgg ctg tct cag ggg agg aac ctg atg cag tgg gtc 2112
388 Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val
390          690          695          700
394 ccg tcc ctg cag ctg ctg ctg cag cca cac tct ctg gag tcc ctc cac 2160
396 Pro Ser Leu Gln Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His
398 705          710          715          720
402 tgc ttg tac gag act cgg aac aaa acg ttc ctg aca caa gtg atg gcc 2208
404 Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala
406          725          730          735
410 cat ttc gaa gaa atg ggc atg tgt gta gaa aca gac atg gag ctc tta 2256
412 His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu
414          740          745          750
418 gtg tgc act ttc tgc att aaa ttc agc cgc cac gtg aag aag ctt cag 2304
420 Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln
422          755          760          765
426 ctg att gag ggc agg cag cac aga tca aca tgg agc ccc acc atg gta 2352
428 Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val
430          770          775          780
434 gtc ctg ttc agg tgg gtc cca gtc aca gat gcc tat tgg cag att ctc 2400
436 Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu
438 785          790          795          800
442 ttc tcc gtc ctc aag gtc acc aga aac ctg aag gag ctg gac cta agt 2448
444 Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser
446          805          810          815
450 gga aac tcg ctg agc cac tct gca gtg aag agt ctt tgt aag acc ctg 2496
452 Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu
454          820          825          830
458 aga cgc cct cgc tgc ctc ctg gag acc ctg cgg ttg gct ggc tgt ggc 2544
460 Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly
462          835          840          845
466 ctc aca gct gag gac tgc aag gac ctt gcc ttt ggg ctg aga gcc aac 2592
468 Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn
470          850          855          860
474 cag acc ctg acc gag ctg gac ctg agc ttc aat gtg ctc acg gat gct 2640
476 Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala
478 865          870          875          880
482 gga gcc aaa cac ctt tgc cag aga ctg aga cag ccg agc tgc aag cta 2688
484 Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu
486          885          890          895
490 cag cga ctg cag ctg gtc agc tgt ggc ctc acg tct gac tgc tgc cag 2736
492 Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln
494          900          905          910
498 gac ctg gcc tct gtg ctt agt gcc ccc agc ctg aag gag cta gac 2784
500 Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp

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Input Set : A:\66821-281

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510      930      935      940
514 ggg ctc agg cat cct gcc tgc aaa ctc ata cgc ctg ggg ctg gac cag 2880
516 Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln
518 945      950      955      960
522 aca act ctg agt gat gag atg agg cag gaa ctg agg gcc ctg gag cag 2928
524 Thr Thr Leu Ser Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln
526      965      970      975
530 gag aaa cct cag ctg ctc atc ttc agc aga cgg aaa cca agt gtg atg 2976
532 Glu Lys Pro Gln Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met
534      980      985      990
538 acc cct act gag ggc ctg gat acg gga gag atg agt aat agc aca tcc 3024
540 Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser
542      995      1000      1005
546 tca ctc aag cgg cag aga ctc gga tca gag agg gcg gct tcc cat gtt 3072
548 Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His Val
550      1010      1015      1020
554 gct cag gct aat ctc aaa ctc ctg gac gtg agc aag atc ttc cca att 3120
556 Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe Pro Ile
558 1025      1030      1035      1040
562 gct gag att gca gag gaa agc tcc cca gag gta gta ccg gtg gaa ctc 3168
564 Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val Glu Leu
566      1045      1050      1055
570 ttg tgc gtg cct tct cct gcc tct caa ggg gac ctg cat acg aag cct 3216
572 Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr Lys Pro
574      1060      1065      1070
578 ttg ggg act gag gat gac ttc tgg ggc ccc acg ggg cct gtg gct act 3264
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586 gag gta gtt gac aaa gaa aag aac ttg tac cga gtt cac ttc cct gta 3312
588 Glu Val Val Asp Lys Glu Lys Asn Leu Tyr Arg Val His Phe Pro Val
590      1090      1095      1100
594 gct ggc tcc tac cgc tgg ccc aac acg ggt ctc tgc ttt gtg atg aga 3360
596 Ala Gly Ser Tyr Arg Trp Pro Asn Thr Gly Leu Cys Phe Val Met Arg
598 1105      1110      1115      1120
602 gaa gcg gtg acc gtt gag att gaa ttc tgt gtg tgg gac cag ttc ctg 3408
604 Glu Ala Val Thr Val Glu Ile Glu Phe Cys Val Trp Asp Gln Phe Leu
606      1125      1130      1135
610 ggt gag atc aac cca cag cac agc tgg atg gtg gca ggg cct ctg ctg 3456
612 Gly Glu Ile Asn Pro Gln His Ser Trp Met Val Ala Gly Pro Leu Leu
614      1140      1145      1150
618 gac atc aag gct gag cct gga gct gtg gaa gct gtg cac ctc cct cac 3504
620 Asp Ile Lys Ala Glu Pro Gly Ala Val Glu Ala Val His Leu Pro His
622      1155      1160      1165
626 ttt gtg gct ctc caa ggg ggc cat gtg gac aca tcc ctg ttc caa atg 3552
628 Phe Val Ala Leu Gln Gly Gly His Val Asp Thr Ser Leu Phe Gln Met
630      1170      1175      1180

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/828,920A

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Input Set : A:\66821-281

Output Set: N:\CRF4\08302004\J828920A.raw

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VERIFICATION SUMMARY

DATE: 08/30/2004

PATENT APPLICATION: **US/10/828,920A**

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